



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/509,145

DATE: 10/05/2004
TIME: 10:53:57

Input Set : A:\82308.sequence
Output Set: N:\CRF4\10052004\J509145.raw

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3 <110> APPLICANT: Epigenomics AG
5 <120> TITLE OF INVENTION: Method for the analysis of methylation patterns within
nucleic acids
6 by means of mass spectrometry.
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/509,145
C--> 8 <141> CURRENT FILING DATE: 2004-09-27
W--> 0 <130> FILE REFERENCE:
8 <160> NUMBER OF SEQ ID NOS: 3
10 <210> SEQ ID NO: 1
11 <211> LENGTH: 17
12 <212> TYPE: DNA
13 <213> ORGANISM: Homo Sapiens
15 <400> SEQUENCE: 1
17 ttgcgtggag tttcgcc
19 <210> SEQ ID NO: 2
20 <211> LENGTH: 18
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo Sapiens
24 <400> SEQUENCE: 2
26 gcttggggga atagggag
28 <210> SEQ ID NO: 3
29 <211> LENGTH: 22
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo Sapiens
33 <400> SEQUENCE: 3
35 aacacgggca ttgatctgac gt

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ENTERED

17

18

22

BEST AVAILABLE COPY

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/509,145

DATE: 10/05/2004

TIME: 10:53:58

Input Set : A:\82308.sequence

Output Set: N:\CRF4\10052004\J509145.raw

L:8 M:270 C: Current Application Number differs, Replaced Current Application No

L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE